What is Claimed is:

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1. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotypes shown in the table immediately below defines one copy of the individual's TNFRSF1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS18 on at least one copy of the individual's TNFRSF1A gene, and wherein each of the TNFRSF1A haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

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10 15 15 16 16 16 16 16 16 16 16 16 16 16 16 16 1	1 G G A C A G C G T C C A A C C C G	2	3	PLOT 5 G G A C A G C G T C C G A T C C G	6 7 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	GACGGCATCCGGCCTG	9 6 6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	10 GGACGGCGTCCGACCCG	NUME	1 2 3 4 5 6 7 8 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		3102 3409 3438 3603 4054 4082 1199 1235 1248 1265 1482 1499 1508 1509 1552 1593	8 6 7 9 3 4 0 9 3 9 2	
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1.130	11	12		PLOT 14	15	NUMB 16	EK 17	18	19	20	VILIM	PS IBER	PS POSITION ^c	
	G G A	G G A	G G A	G G A	G G G	G G G	G G G	G T A	G T A	G T A	NON	1 2 3	3102 3409 3438	
35	CGGC	C G G C	C G G C	C G T	C A G C	C A G C	C A G T	C A A C	C A G C	C A G C		5 6 7	3603 4054 4082 11998	
40	G T C C	G T C C	G T C T	G T C C	G T C C	G T C C	G T C	G T C T	G T C C	G T C C		8 \ 9 10 11	12356 12397 12489 12653	
45	G A C	G G C	G A C	G G C	G A C	G A C	G A C	G A C	G A C	G G C		12 13 14	14824 14990 15089	
	C T G G	C T G G	C T G G	C T G G	C C G G	C T G G	C C G G	C T G G	C T A G	C T G G		15 16 17 18	15093 15529 15932 16165	
50													1	

			HA	PLOT	YPE	NUMB	ER ^a		PS ^b	PS
	21	22	23	24	25	26	27		NUMBER	POSITIONC
	G	G	G	∖ G -	G	G	${f T}$		1	3102
	\mathbf{T}	${f T}$	\mathbf{T}	Ì	T	${f T}$	G .		2	3409
5	A	A	A	A	A	G	G		3	3438
	С	С	С	C /	√ G	С	C		4	3603
	A	A	A	G	\A	A	A		5	4054
	G	G	G	G	Ġ	G	G		6	4082
	С	С	С	С	c /	C	С		7	11998
10	G	G	G	G	G	∖ G	G		8	12356
	T	\mathbf{T}	${f T}$	${f T}$	T	Z	\mathbf{T}		9	12397
	С	С	${ m T}$	C	C	C/	C		10	12489
	\mathbf{T}	\mathbf{T}	\mathbf{T}	${f T}$	\mathbf{T}	c \	C		11	12653
	G	G	G	G	G	G	\ G		12	14824
15	A	A	A	A	A	A	\$\frac{1}{2}		13	14990
	C	С	С	С	С	С	c/		14	15089
	С	С	C	С	С	С	c /		15	15093
	С	\mathbf{T}	${ m T}$	${f T}$	${f T}$	С	T		16	15529
	G	G	G	G	G	G	G \	\	17	15932
2 0	G	G	G	G	G	G	A	\	18	16165

^aAlleles for haplotypes are presented 5 to 3' in each column

2. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS18 on both copies of the individual's TNFRSF1A gene, and wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

^bPS = polymorphic site;

^cPosition of PS within SEQ ID NO:1.

ş.	5	HAPLOT 12/12 G/G G/G A/A C/C G/G	TYPE PA 22/22 G/G T/T A/A C/C A/A G/G	IR ^a 2/2 G/G G/G A/A C/C A/A G/G	22/20 G/G T/T A/A C/C A/A G/G	12/10 G/G G/G A/A C/C G/G	2/1 G/G G/G A/A C/C A/A G/G	22/23 G/G T/T A/A C/C A/A G/G	2/11 G/G G/G A/A C/C A/G G/G	PS ^b NUMBER 1 2 3 4 5	PS POSITION° 3102 3409 3438 3603 4054 4082
	10	C/C G/G	C/C G/G	C/C G/G	C/d G/G	C/C G/G	C/C G/G	C/C G/G	C/C G/G	7 8 9	11998 12356 12397
		T/T C/C C/C	T/T C/C T/T	T/T C/C C/C	T/T \ C/C T/C	T/T C/C C/C	T/T C/C C/C	T/T C/T T/T	T/T C/C C/C	10 11 12	12489 12653 14824
548	15	G/G G/G C/C	G/G A/A C/C	G/G A/A C/C	G/G A/G C/C	G/G G/A C/C	G/A A/A C/C	G/G A/A C/C	G/G A/A C/C	13 14	14990 15089
(20)	L,	C/C C/C T/T	C/C T/T	C/C C/C	C/C T/T	C/C T/C	C/C C/C	C/C T/T	C/C C/T	15 16	15093 15529
CON	^2 0	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G G/G	17 18	15932 16165
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	e see engage gene jungah		TYPE PA 3/14	AIR ^a 12/1	5 22/8	2/9	3/21	2/15	12/17	PS ^D NUMBER	PS POSITION ^c
	25	2/19	3/14	12/1	5 22/8 G/G	2/9 G/G	3/21 G/G	2/15 G/G	12/17 G/G		POSITION ^c 3102
		2/19 G/G	3/14 G/G	AIR ^a 12/1 G/G G/G	5 22/8 G/G T/G				G/G G/G	NUMBER 1 2	POSITION° 3102 3409
	THE REAL PROPERTY OF THE PROPE	2/19 G/G G/T	3/14	12/1 G/G	G/G	G/G	G/G\	G/G G/G ∖A/G	G/G G/G A/G	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
	the state of the s	2/19 G/G	3/14 G/G G/G	12/1 G/G G/G	G/G T/G	G/G G/G	G/G G/T A/A C/C	G/G G/G A/G C/C	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
	45	2/19 G/G G/T A/A	3/14 G/G G/G A/A	12/1 G/G G/G A/G	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
	45	2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/1 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/G G/T A/A C/C A/A G/G	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
	45	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/1 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
	45	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/1 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A GXG C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/1 G/G G/G A/G C/C G/A G/G C/C G/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
ı		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C	12/1 G/G G/G A/G C/C G/A G/G C/C G/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/G	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/C G/A T/C C/C G/G	G/G G/G A/A C/C A/G G/G C/C G/C C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G	G/G G/G A/C G/A G/G G/T G/C C/C G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/G A/G	12/1 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G G/A	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/G	G/G G/G A/A C/C A/G G/C G/C C/C G/C C/C A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/G A/A	G/G G/G A/G C/C A/A G/G G/G T/T C/C C/C G/G A/A	G/G G/G A/G C/C G/A G/G C/T G/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T C/C G/G A/G C/C	12/1 G/G G/G A/G C/C G/A G/C C/C G/G T/T C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/A T/C G/G A/G C/C	G/G G/G A/A C/C A/G G/C G/C C/C G/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/C C/A G/G C/T C/C G/G G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
	The second secon	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	3/14 G/G G/G A/A C/C A/G G/T C/C G/G T/T C/C G/G C/C	12/1 G/G G/G A/C G/A G/C G/G T/T C/C G/A C/C C/C	G/G T/G A/A C/C G/G C/A T/C G/G C/C A/C C/C	G/G G/G A/A C/C A/G G/C G/C C/C G/A C/C C/C	G/G G/T A/A C/C A/A G/C G/G T/T C/T G/A C/C	G/G G/G A/A C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/C A/C G/A G/T C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
		2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C C/C C/T	3/14 G/G G/G A/A C/C A/G G/G C/T C/C G/G C/C G/C T/T	12/1 G/G G/G A/G C/C G/A G/G C/C G/G G/A C/C C/C C/C T/C	G/G T/A C/C A/G C/A T/C G/G C/C T/T	G/G G/G A/A C/C A/G G/C G/C C/C G/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/C A/C G/A G/T C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932
	The second secon	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	3/14 G/G G/G A/A C/C A/G G/T C/C G/G T/T C/C G/G C/C	12/1 G/G G/G A/C G/A G/C G/G T/T C/C G/A C/C C/C	G/G T/G A/A C/C G/G C/A T/C G/G C/C A/C C/C	G/G G/G A/A C/C A/G G/C C/C G/C C/C C/C C/T	G/G G/T A/A C/C A/A G/C G/G T/T C/T G/A C/C T/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/C C/C	G/G G/G A/C G/G G/T C/C G/A CC T/C CG/A CT	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

		HAPLOT	YPE\PA	IRª						PS^b	PS
		2/21	22/3		512/25	12/24	12/13	3/16	22/16	NUMBER	POSITIONC
		G/G	G/G \	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
		G/T	T/G \	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
	5	A/A	A/A	\A/A	A/A	A/A	A/A	A/G	A/G	3	3438 .
İ		C/C	C/C	द ∕G	C/G	C/C	C/C	C/C	C/C	4	3603
		A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
<u> </u>		G/G	G/G	GλG	G/G	G/G	G/G	G/G	G/G	6	4082
		C/C	C/C	c/ <i>q</i>	C/C	C/C	C/C	C/C	C/C	7	11998
	10	G/G	G/G	G/G\	G/G	G/G	G/G	G/G	G/G	8	12356
ļ		T/T	T/T	T/T \	\T/T	T/T	T/T	T/T	\mathbb{T}/\mathbb{T}	9	12397
		C/C	C/C	C/C	¢\c	C/C	C/C	C/C	C/C	10	12489
		C/T	T/C	T/T	СVТ	C/T	C/T	C/C	T/C	11	12653
1 . A		G/G	G/G	G/G	G ∕ G	G/G	G/G	G/G	G/G	12	14824
1346	15	A/A	A/A	A/A	G/A\	G/A	G/A	A/A	A/A	13	14990
` ,		C/C	C/C	C/C	c/c \	C/C	C/C	C/C	C/G	14	15089
101		C/C	C/C	C/C	c/c \	C/C	C/C	C/C	C/C	15	15093
I FI		C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
1000	•	G/G	G/G	G/G	G/G	Ğ ∕G	G/G	G/G	G/G	17	15932
Co	20	G/G	G/G	G/G	G/G	GΧG	G/G	G/G	G/G	18	16165
1	Saleh.					*					
ļ		HADI O	יעטב טא	тра	•	1				Dap	DQ
			TYPE PA		2/26	22/11	12/7	22/2	22/18	PS ^b	PS POSITION ^C
ı		3/27	22/10	2/16	2/26 G/G	22/11	12/7 G/G	22/2 G/G	22/18 G/G	NUMBER	${\tt POSITION}^{\tt c}$
		3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	√G/G	G/G	G/G	NUMBER 1	POSITION° 3102
		3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	G/G T/G	G/G T/T	NUMBER 1 2	POSITION ^c 3102 3409
		3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G AXA	G/G T/G A/A	G/G T/T A/A	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
		3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G AXA C/C	G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION° 3102 3409 3438 3603
	lji	3/27 G/T G/G A/G C/C A/A	22/10 G/G T/G A/A C/C A/G	2/16 G/G G/G A/G C/C A/A	G/G G/T A/G C/C A/A	G/G T/G A/A C/C A/G	G/G G/G AXA C/C G/A	G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3 4 5	POSITION° 3102 3409 3438 3603 4054
	lji	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G AXA C/C G/A G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
	lji	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G AXA C/C G/A G/G C/C	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
	lji	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G AXA C/A G/G G/C G/C	G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
	lji	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G AXA C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
		3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G AXA C/A G/G G/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
		3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T CXC	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
	lji	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/C C/C G/G T/T C/C G/G	G/G G/G A/A C/A G/G C/C G/T C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
		3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G G/G A/G C/C A/A G/C G/G T/T C/C G/G A/A	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A	G/G G/G A/A C/A G/C G/G T/T C/C G/G G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/C G/G A/A	G/G T/T A/A C/C A/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
		3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/C C/C G/G T/T C/C G/G	G/G G/G A/A C/A G/G C/C G/T C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
		3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/C G/G T/T C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G A/A C/C	G/G T/A C/C A/C G/C G/C G/T C/C G/A C/C	G/G G/A C/A G/C G/T C/G G/C G/C C/C G/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C A/A C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
		3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/G C/C A/A G/C G/G T/T C/C G/A C/C	G/G G/T A/C A/A G/C G/G T/C C/C G/A C/C	G/G T/A C/C A/C G/C G/C T/C C/C G/A C/C C/C	G/G G/A G/A G/C G/T C/G G/C C/C C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/T A/A C/C A/A G/A C/G T/T C/T G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
	ment and the state of the state	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C G/C A/A C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/A C/C C/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/A C/C C/C	G/G T/G A/A C/C A/G G/C G/T T/C G/A C/C T/T	G/G G/GA C/A C/A C/G/G C/C G/G C/C T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C A/A C/C T/C	G/G T/T A/A C/A G/A G/C G/G T/T C/C T/T G/A C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

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HAPLOT	YPE PA	IR ^a				PS ^b	PS
22/12	12/5\	12/3	12/2	14/6	16/4	NUMBER	POSITIONC
G/G	G/G \	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	\ G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	C/C	cXc	C/C	C/C	C/C	4	3603
A/G	G/A	G/À	G/A	G/A	A/A	5	4054
G/G	G/G	G/G\	G/G	G/G	G/G	6	4082
C/C	C/C	C/C \	\C/C	T/C	C/C	7	11998
G/G	G/G	G/G	ð√G	G/G	G/G	8	12356
T/T	T/T	T/T	т Хт	T/T	T/T	9	12397
C/C	C/C	C/C	c\ <i>q</i>	C/C	C/C	10	12489
T/C	C/C	C/C	c/c\	C/C	C/C	11	12653
G/G	G/G	G/G	G/G \	G/G	G/G	12	14824
A/G	G/A	G/A	G/A \	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	℃ /c	C/C	14	15089
C/C	C/C	C/C	C/C	cXc	C/T	15	15093
T/T	T/C	T/T	T/C	\mathbb{Z}/\mathcal{C}	T/C	16	15529
G/G	G/G	G/G	G/G	G/G\	G/G	17	15932
G/G	G/G	G/G	G/G	G/G \	G/G	18	16165

^aHaplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column; ^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1.

- 3. A method for genotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, comprising determining for the two copies of the TNFRSF1A gene present in the individual the identity of the nucleotide pair at one or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the one or more PS have the position and alternative alleles shown in SEQ ID NO:1.
- 4. The method of claim 3, wherein the determining step comprises:
 - (a) isolating from the individual a nucleic acid mixture comprising both copies of the TNFRSF1A gene, or a fragment thereof, that are present in the individual;
 - (b) amplifying from the nucleic acid mixture a target region containing one of the selected polymorphic sites;
 - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for genotyping the selected polymorphic site in the target region;
 - (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
 - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.

- 5. The method of claim 3, which comprises determining for the two copies of the TNFRSF1A gene present in the individual the identity of the nucleotide pair at each of PS1-PS18.
- 6. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual which comprises determining, for one copy of the TNFRSF1A gene present in the individual, the identity of the nucleotide at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 7. The method of claim 6, further comprising determining the identity of the nucleotide at one or more polymorphic sites selected from the group consisting of PS2, PS3, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS13 and PS16, which has the location and alternative alleles shown in SEQ ID NO: 1.
- 8. The method of claim 6, wherein the determining step comprises:
 - (a) isolating from the individual a nucleic acid sample containing only one of the two copies of the TNFRSF1A gene, or a fragment thereof, that is present in the individual;
 - (b) amplifying from the nucleic acid sample a target region containing one of the selected polymorphic sites;
 - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for haplotyping the selected polymorphic site in the target region;
 - (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
 - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.
- 9. A method for predicting a haplotype pair for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual comprising:
 - (a) identifying a TNFRSF1A genotype for the individual, wherein the genotype comprises the nucleotide pair at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1;
 - (b) comparing the genotype to the haplotype pair data set forth in the table immediately below; and
 - (c) determining which haplotype pair is consistent with the genotype of the individual and with the haplotype pair data

	HAPLOT	TYPE PA	.IRª						PS ^b	PS
	12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITIONC
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
15	G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G .	2	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
20	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
	C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
25	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
	G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
	T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
30	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
Land Land	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
7.4										
. 479										
		YPE PA							PS ^b	PS
	2/19	3/14	12/15	5 22/8	2/9	3/21	2/15	12/17	NUMBER	POSITION°
	2/19 G/G	3/14 G/G	12/15 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
	2/19 G/G G/T	3/14 G/G G/G	12/15 G/G G/G	G/G T/G	G/G G/G	G/G G/T	G/G G/G	G/G G/G	NUMBER 1 2	POSITION° 3102 3409
San	2/19 G/G G/T A/A	3/14 G/G G/G A/A	12/15 G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/G G/T A/A	G/G G/G A/G	G/G G/G A/G	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
	2/19 G/G G/T A/A C/C	3/14 G/G G/G A/A C/C	12/15 G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G G/T A/A C/C	G/G G/G A/G C/C	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
	2/19 G/G G/T A/A C/C A/A	3/14 G/G G/G A/A C/C A/G	12/15 G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
	2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/15 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/G G/T A/A C/C A/A G/G	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/15 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
State of the state	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
Special plane in the state of t	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
State of the state	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/C C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
Special plane in the state of t	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G	G/G G/G A/A C/C A/G G/C C/C C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
Special plane in the state of t	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G	12/15 G/G G/G A/G C/C G/A G/G C/C C/C G/G T/T C/C C/C G/A	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/G	G/G G/G A/A C/C A/G G/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/G A/G C/C G/A G/G C/T G/C C/C G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
Special plane in the state of t	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/A T/T C/C G/G A/C C/C	G/G G/G A/A C/C A/G G/C C/C G/G T/C C/C G/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C G/G G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
The property of the property o	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/C C/C	12/15 G/G G/G A/G C/C G/A G/C C/C C/C C/C C/C C/C C/C	G/G T/A C/C A/C G/C C/A T/C C/C G/C C/C C/C	G/G G/G A/A C/C A/G G/C C/C C/C G/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/C C/C G/A G/G T/T C/C G/G G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
Special plane in the state of t	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	3/14 G/G G/G A/A C/C A/G G/G T/T C/C G/G A/C C/C T/T	12/15 G/G G/G A/G C/C G/A G/C C/C G/G T/T C/C C/C G/A C/C T/C	G/G T/A C/C A/G G/C A/T C/C G/G C/C T/T C/C T/T	G/G G/G A/C A/C G/C C/C G/C C/C C/C C/T	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/G A/C C/C G/A G/G T/T C/C G/A C/C C/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15089 15093
The property of the property o	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/C C/C	12/15 G/G G/G A/G C/C G/A G/C C/C C/C C/C C/C C/C C/C	G/G T/A C/C A/C G/C C/A T/C C/C G/C C/C C/C	G/G G/G A/A C/C A/G G/C C/C C/C G/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/C C/C G/A G/G T/T C/C G/G G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093

	HAPLO	TYPE PA	IRa						PS ^b	PS
55	2/21	22/3		5 12/25	12/24	12/13	3/16	22/16	NUMBER	POSITION°
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
2	G/T	T/G	T/T	G./T	G/T	G/G	G/G	T/G	2	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
	C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
60	A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
65	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
	C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
	A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
70	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
	c/c .	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
E Z	_, -	-, -	-, -	-, -	_, _	-, -	-, -	-, -		
75	HAPLOT	TYPE PA	IR^{a}						PS ^b	PS
75	HAPLOT	TYPE PA 22/10	IR ^a 2/16	2/26	22/11	12/7	22/2	22/18	PS ^b NUMBER	PS POSITION ^c
				2/26 G/G	22/11 G/G	12/7 G/G	22/2 G/G	22/18 G/G		
75 U1	3/27	22/10	2/16						NUMBER	POSITION°
75	3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
50 80	3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	G/G T/G	G/G T/T	NUMBER 1 2	POSITION ^c 3102 3409
80	3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G A/A	G/G T/G A/A	G/G T/T A/A	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
80	3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
80	3/27 G/T G/G A/G C/C A/A	22/10 G/G T/G A/A C/C A/G	2/16 G/G G/G A/G C/C A/A	G/G G/T A/G C/C A/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C G/A	G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
80	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C G/A G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
80	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C G/A G/G C/C	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
80	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
genera grub, general grub, grub, servet, action grub, action grub, grub, servet, action grub, ac	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A	G/G G/G A/A C/C G/A G/C G/C G/C C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
genera grub, general grub, grub, servet, action grub, action grub, grub, servet, action grub, ac	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/C A/A G/C C/C G/G T/T C/C G/G A/A C/C C/T	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/A C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C	G/G G/G A/A C/C G/A G/C G/C C/C G/C C/C G/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
genera grub, general grub, grub, servet, action grub, action grub, grub, servet, action grub, ac	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/A G/C G/G T/T C/C G/G A/A C/C	G/G G/T A/C A/C G/C G/C T/C C/C A/C C/C C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C	G/G G/A C/A C/A G/G C/C G/G C/C C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/T G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
general level leve	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/C A/A G/C C/C G/G T/T C/C G/G A/A C/C C/T	G/G G/T A/C A/C G/C G/C T/C C/C G/A C/C C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/A C/C T/T	G/G G/G A/A C/C G/A G/C G/C C/C G/C C/C C/C T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G T/T A/A C/C A/A G/A C/G T/T C/T G/A C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
genera grub, general grub, grub, servet, action grub, action grub, grub, servet, action grub, ac	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C T/T G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C G/G	2/16 G/G G/G A/C A/G C/C G/T C/C G/A C/C C/T G/G	G/G G/T A/G C/A G/C G/T C/C G/A C/C G/G A/C C/C G/G	G/G T/A C/C A/G G/C G/C T/T C/C G/A C/C T/T G/G	G/G G/G A/A C/C G/A G/C G/C C/C G/C C/C G/C C/T G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C T/C G/G	G/G T/T A/A C/C A/A G/G T/T C/C T/T G/A C/C T/T G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15089 15093 15529

	HAPL(TYPE PA	AIR ^a				PS ^b	PS
	22/12		12/3	12/2	14/6	16/4	NUMBER	POSITION°
	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	T/G	G/G	G/G	G/G	G/G	G/G	2	3409
100	A/A	A/A	A/A	A/A	A/A	G/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	A/G	G/A	G/A	G/A	G/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
	C/C	C/C	C/C	C/C	T/C	C/C	7 .	11998
105	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
	T/C	C/C	C/C	C/C	C/C	C/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
110	A/G		G/A	G/A	G/G	A/A	13	14990
	C/C	C/T	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/T	15	15093
	T/T	T/C	T/T	T/C	T/C	T/C	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	17 18	15932 16165
1 1.5	G/G	G/G	G/G	G/G	G/G	G/G	10	10102
1.00 mg		arr1 . 4			mtad aa 1 st	hanlatun	o/2nd hanlats	pe; with allele
120 120		Haplotype	pairs ar	e represe st polymo	med as 1	napiotyp odvmo	e/2 Haptoty	ach column;
eliee		snown 5 t ^b PS = poly			npmsm/2	porymo	ipinsiii iii ca	acii coluilii,
120		Position c			IO·1			
187		r osmon c	u i S iii S	EQ ID I	10.1.			
	10. T	he method	of claim	9, where	in the ide	ntified ge	notype of th	e individual co
F	n	ucleotide p	air at eac	h of PS1	-PS18, wl	hich have	the position	and alternativ
1220 1220	Q	EQ ID NO	-1					
		_						. 1
id.				_				t least one hap
5	p	air of the t	ımor nec	rosis fac	tor recepto	or superfa	mily, memb	er 1A (TNFRS
in i	c	omprises c	omparing	g the freq	uency of	the haplot	ype or haplo	otype pair in a

^aHaplotype pairs are represented as 1^{st} haplotype/ 2^{nd} haplotype; with alleles of each haplotype shown 5' to 3' as 1^{st} polymorphism/ 2^{nd} polymorphism in each column; ^bPS = polymorphic site;

- The method of claim 9, wherein the identified genotype of the individual comprises the 10. nucleotide pair at each of PS1-PS18, which have the position and alternative alleles shown in SEQ ID NO:1.
- A method for identifying an association between a trait and at least one haplotype or haplotype 11. pair of the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene which comprises comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, wherein the haplotype is selected from haplotypes 1-27 shown in the table presented immediately below, wherein each of the haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

				HA]	PLO:	CYPE	ı N	UMB1	ΣR ^a		Ι	2S ^b	PS	
	1	2	3	4	5	6	7	8	9	10	NUMB	ER	POSI	TION ^c
	G	G	G	G	G	G	G	G	G	G		L	3102	
15	G	G	G	G	G	G	G	G	G	G		2	. 3409	
	A	Α	A	Α	A	A	Α	A	A	A		3	3438	
	С	С	С	С	C	С	С	С	С	С		4	3603	
	A	A	A	A	A	A	Α	G	G	G		5	4054	
	G	G	G	G	G	G	G	G	G	G		ố .	4082	
20	С	С	С	С	C	C	С	С	С	С		7	1199	
	G	G	G	G	G	G	G	A	G	G		3	1235	
	\mathbf{T}	${f T}$	\mathbf{T}	${ m T}$	\mathbf{T}	Т	Т	T	С	\mathbf{T}		9	1239	
	С	С	С	C	С	С	С	С	С	С		10	1248	
	С	С	С	C	С	С	С	С	С	С		11	1265	
25	A	G	G	G	G	G	G	G	G	G		12	1482	
	A	A	A	Α	A	G	G	G	A	A		13	1499	
	С	C	С	С	\mathbf{T}	С	C	C	C	C		14	1508	
	С	С	С	T	С	С	С	C	C	C		15	1509	
	С	С	T	С	С	С	T	T	T	C		16	1552	
30	G	G	G	G	G	G	G	, G	G	G		17	1593	
40000	G	G	G	G	G	G	G	G	G	G		18	1616	5
P. Sant														
				T 7 7 7	TO T ()	TI SUID I	דא י	T T N AT T >	m Da				Dap	DC
militar Faller F	11	7	2			TYPE		UMB		10	10	20	PS ^b	PS POSITION ^C
	11		2	13	14	1	5	16	17	18 G	19 G	20 G	NUMBER	POSITIONC
The Reserved Profession	G	G	;	13 G	14 G	1 G	5	16 G	17 G	G	G	G	NUMBER 1	POSITION° 3102
	G G	G	;	13 G G	14 G G	1 G G	5	16 G G	17 G G	G T	G T	G T	NUMBER 1 2	POSITION ^c 3102 3409
	G G A	G A	; ;	13 G G A	14 G G A	1 G G G	5	16 G G G	17 G G G	G T A	G T A	G T A	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
E.	G G A C	G G A C	; ;	13 G G A	14 G G A C	1 G G G C	5	16 G G G	17 G G G C	G T A C	G T A C	G T A C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
E.	G G A C G	G A C G		13 G G A C	14 G G A C	1 G G C A	5	16 G G G C A	17 G G C A	G T A C A	G T A C A	G T A C A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438
E.	G G A C G	G A C G		13 G G A C G	14 G A C G	1 G G C A G	5	16 G G C A G	17 G G C A G	G T A C A	G T A C	G T A C A G	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603 4054
	G A C G C	G G A C G G		13 G G A C G G	14 G A C G G	1 G G C A G	5	16 G G G C A	17 G G C A G T	G T A C A	G T A C A G	G T A C A G	NUMBER 1 2 3 4 5	POSITION° 3102 3409 3438 3603 4054 4082
Marie gener general News 128 (1997)	G G C G C G	G G A C G G		13 G G A C G	14 G G A C G G T	1 G G C A G C	5	16 G G G C A G	17 G G C A G	G T A C A A	G T A C A G C	G T A C A G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
	G G A C G G C G T	G G A C G G		13 G G A C G G G	14 G A C G G	1 G G C A G	5	16 G G C A G C	17 G G C A G T	G T A C A C G	G T A C A G C G	G T A C A G C G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
Marie gener general News 128 (1997)	G G C G C G	G A C G C C		13 G G A C G G C G	14 G G A C G G T	1 GGGCA GCG T	5	16 G G C A G C T	17 G G C A G T G T	G T A C A C G T	G T A C A G C G T	G T A C A G C G T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
	G A C G C G T C	G A C G G C T		13 G G A C G G C G T C	14 G A C G G T C	1 G G C A G C G T C	5	16 G G C A G C G T C	17 GGGCAGTGTC	G T A C A A C G T C	G T A C A G C G T C	G T A C A G C G T C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
	G G A C G G C G T C C	G G G G C C		13 G G A C G G C G T C T	14 G A C G G T C C	1 G G C A G C G T C C	5	16 GGGCAGCGTCC	17 GGGCAGTGTCC	G T A C A A C G T C T	G T A C A G C G T C C	G T A C A G C G T C C G G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
	G G A C G G C G T C C G A C	G G G G G G C C		13 G G A C G G C G T C T G	14 G A C G G T C C G G C	1 G G G C A G C G T C C G A C	5	16 GGGCAGCGTCCGAC	17 GGGCAGTGTCCGAC	G T A C A A C G T C T G A C	G T A C A G C G T C C G A C	G T A C A G C G T C C G G C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
45	G G A C G G C G T C C G A C C	G G G G G G G G G G G G G G G G G G G		13 GGACGGCGTCTGACC	14 G G A C G G T G T C C G G C C	1 G G G C A G C G T C C G A C C	5	16 GGGCAGCGTCCGACC	17 GGGCAGTGTCCGACC	G T A C A A C G T C T G A C C	G T A C A G C G T C C G A C C	G T A C A G C G T C C G G C C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
	G G A C G G C G T C C G A C C T	G G G A A C G G G G G G G G G G G G G G		13 GGACGGCGTCTGACCT	14 G G A C G G T G T C C G G C C T	1 G G G C A G C G T C C G A C C C	5	16 GGGCAGCGTCCGACCT	17 GGGCAGTGTCCGACCC	G T A C A A C G T C T G A C C T	G T A C A G C G T C C G A C C T	G T A C A G C G T C C G G C C T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
45	G G A C G G C G T C C G A C C	G G G G G G G G G G G G G G G G G G G		13 GGACGGCGTCTGACC	14 G G A C G G T G T C C G G C C	1 G G G C A G C G T C C G A C C	5	16 GGGCAGCGTCCGACC	17 GGGCAGTGTCCGACC	G T A C A A C G T C T G A C C	G T A C A G C G T C C G A C C	G T A C A G C G T C C G G C C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093

			HA	PLOT	YPE	NUMB	ER ^a		PS ^b	PS
55	21	22	23	24	25	26	27		NUMBER	POSITION°
	G	G	G	G	G	G	T		1	3102
	\mathbf{T}	\mathbf{T}	T	\mathbf{T}	${f T}$	${f T}$	G		2	3409
	A	Α.	A	A	A	G	G		3	3438
	С	C	C	С	G	С	C		4	3603
60	A	A	Α	G	A	A	A		5	4054
	G	G	G	G	G	G	G		6	4082
	С	С	С	С	C	С	С		7	11998
	G	G	G	G	G	G	G		8	12356
	T	${f T}$	${f T}$	\mathbf{T}	\mathbf{T}	\mathbf{T}	\mathbf{T}		9	12397
65	С	С	T	С	С	С	C		10	12489
	\mathbf{T}	\mathbf{T}	${ m T}$	${f T}$	\mathbf{T}	С	C		11	12653
	G	G	G	G	G	G	G		12	14824
	A	A	A	A	A	A	Α		13	14990
	С	С	C	С	С	С	C		14	15089
70	С	С	С	С	C	С	С		15	15093
	С	\mathbf{T}	${f T}$	${f T}$	\mathbf{T}	С	T		16	15529
	G	G	G	G	G	G	G		17	15932
garang Lancor	G	G	G	G	G	G	A		18	16165
Trune Co		3 4 11		1	1 ,			. 151. 0	/ · 1 1	

^aAlleles for haplotypes are presented 5' to 3' in each column;

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

and wherein the haplotype pair is selected from the haplotype pairs shown in the table immediately below, wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

	HAPLOT	TYPE PA	IR ^a						PS ^b	PS
	12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION°
85	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2 .	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
90	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
95	C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
	G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
100	T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
AUTOS (Single No Colon France	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
Annual frame of the second sec	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
13000										
2.2.3	בו א דור הי	TVDE DA	TDa						PS ^b	PS
105		TYPE PA	IR ^a 12/1	5 22 /8	2/9	3/21	2/15	12/17	PS ^b NUMBER	PS POSITION°
105	2/19	3/14	12/1	5 22/8 G/G	2/9 G/G	3/21 G/G	2/15 G/G	12/17 G/G	NUMBER	POSITIONC
1 05	2/19 G/G	3/14 G/G	12/1: G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
105	2/19 G/G G/T	3/14 G/G G/G	12/1: G/G G/G	G/G T/G	G/G G/G	G/G G/T	G/G G/G	G/G G/G	NUMBER 1 2	POSITIONC
105	2/19 G/G G/T A/A	3/14 G/G G/G A/A	12/1: G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/G G/T A/A	G/G G/G A/G	G/G G/G A/G	NUMBER 1	POSITION ^c 3102 3409
man pung guan man di dang man di dang	2/19 G/G G/T A/A C/C	3/14 G/G G/G A/A C/C	12/1: G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G G/T A/A C/C	G/G G/G A/G C/C	G/G G/G	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
Ting the same of t	2/19 G/G G/T A/A C/C A/A	3/14 G/G G/G A/A C/C A/G	12/1: G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A	G/G G/G A/G	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
Ting the same of t	2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/19 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/G G/T A/A C/C	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION° 3102 3409 3438 3603 4054
1 10	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/1: G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A G/G	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G C/T	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
110 145	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
110 145	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
110 145	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/15 G/G G/G A/G C/C G/A G/G C/C C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/G G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
110 145	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C	12/15 G/G G/G A/G C/C G/A G/G C/C G/C G/G T/T C/C C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C C/C G/G A/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C C/C G/G G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
110 145	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G A/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C G/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/C A/C C/C T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C T/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G C/C T/T	G/G G/G A/A C/C A/G G/G C/C G/C C/C C/C C/C C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/A C/C C/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/T G/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/G A/G C/C T/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G G/A C/C C/C G/G G/A	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G A/G C/C T/T G/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C C/C G/G A/A C/C C/T	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/G A/A C/C C/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C G/G	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/G G/A C/C C/C G/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15089 15093 15529 15932
	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/C C/C G/C A/C C/C T/T	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C T/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G C/C T/T	G/G G/G A/A C/C A/G G/G C/C G/C C/C C/C C/C C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/A C/C C/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

125	HAPLO'	TYPE PA	IR ^a						PS ^b	PS
	2/21	22/3		5 12/25	12/24	12/13	3/16	22/16	NUMBER	POSITIONC
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
	A/A	A/A	A/A		A/A	A/A	A/G	A/G	3	3438
130	C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
	A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	g/G	6	4082
	C/C	. C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
135	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	c/c	c/c	C/C	c/c	10	12489
	C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
	A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
140	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
1.0	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
	C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
and the same	-, -	-, -	-, -	-, -	-, -	-, -	-, -	- /		
145										
145	HAPI _O '	TYPE PA	IR ^a						PS ^b	PS
145		TYPE PA 22/10		2/26	22/11	12/7	22/2	22/18		
145	3/27	22/10	2/16	2/26 G/G	22/11 G/G	12/7 G/G	22/2 G/G	22/18 G/G	NUMBER	$POSITION^{c}$
145	3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
145 	3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	G/G T/G	G/G T/T	NUMBER 1 2	POSITION° 3102 3409
150	3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G A/A	G/G T/G A/A	G/G T/T A/A	NUMBER 1	POSITION ^c 3102 3409 3438
150	3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
150	3/27 G/T G/G A/G C/C A/A	22/10 G/G T/G A/A C/C A/G	2/16 G/G G/G A/G C/C A/A	G/G G/T A/G C/C A/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C G/A	G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438
150	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C G/A G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603 4054
150	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C G/A G/G C/C	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
1 50	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 6 7	POSITION° 3102 3409 3438 3603 4054 4082 11998
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
	3/27 G/T G/G A/G C/C A/A G/G C/C G/C G/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
	3/27 G/T G/G A/G C/C A/A G/G C/C G/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A	G/G G/G A/A C/C G/A G/C C/C G/G T/T C/C C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G T/G A/A C/C A/G G/C G/G T/T C/C G/G A/A C/C C/C	G/G G/G A/A C/C G/A G/C C/C G/G T/T C/C G/G G/G C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G G/A C/C G/A G/C G/C G/C G/C C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C T/T G/G A/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093

	HAPLOT	YPE PA	IR ^a				PS ^b	PS
	22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION°
	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
170	T/G	G/G	G/G	G/G	G/G	G/G	2	3409
	A/A	A/A	A/A	A/A	A/A	G/A	3	3438
	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	A/G	G/A	G/A	G/A	G/A	A/A	5	4054
	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
175	C/C	C/C	C/C	C/C	T/C	C/C	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
	T/C	C/C	C/C	C/C	C/C	C/C	11	12653
180	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
	A/G	G/A	G/A	G/A	G/G	A/A	13	14990
	C/C	C/T	C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	C/C	C/T	15	15093
	T/T	T/C	T/T	T/C	T/C	T/C	16	15529
185	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
Sales	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

^aHaplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;

wherein a higher frequency of the haplotype or haplotype pair in the trait population than in the reference population indicates the trait is associated with the haplotype or haplotype pair.

- 12. The method of claim 11, wherein the trait is a clinical response to a drug targeting TNFRSF1A.
- 13. An isolated oligonucleotide designed for detecting a polymorphism in the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene at a polymorphic site (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 14. The isolated oligonucleotide of claim 13, which is an allele-specific oligonucleotide that specifically hybridizes to an allele of the TNFRSF1A gene at a region containing the polymorphic site.
- 15. The allele-specific oligonucleotide of claim 14, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:4-10, the complements of SEQ ID NOS:4-10, and SEQ ID NOS:11-24.
- 16. The isolated oligonucleotide of claim 13, which is a primer-extension oligonucleotide.
- 17. The primer-extension oligonucleotide of claim 16, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:25-38.
- 18. A kit for haplotyping or genotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises a set of oligonucleotides designed to haplotype or genotype each of polymorphic sites (PS) PS1, PS4, PS12, PS14, PS15, PS17 and

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

- PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 19. The kit of claim 18, which further comprises oligonucleotides designed to genotype each of PS2, PS3, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS13 and PS16, having the location and alternative alleles shown in SEQ ID NO:1.
- 20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the TNFRSF1A isogene is selected from the group consisting of isogenes 1-27 shown in the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

											1		
		I	SOG	ENE	NU	MBE	R^a			PS ^b	RS	SEQ ID	REGION
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION°	NO.	$EXAMINED^\mathtt{d}$
G	G	G	G	G	G	G	G	G	G	1	31\02	1	2920-4210
G	G	G	G	G	G	G	G	G	G	2	34 0 ,9	1	2920-4210
Α	Α	Α	A	Α	A	Α	A	A	A	3	3438	1	2920-4210
С	С	С	С	С	С	С	С	С	С	4	3603√	1	2920-4210
А	Α	Α	Α	Α	A	A	G	G	G	5	4054	1	2920-4210
G	G	G	G	G	G	G	G	G	G	6	4082 \	1	2920-4210
С	С	С	С	С	С	С	С	С	С	7	11998 🔪	1	11417-12926
G	G	G	G	G	G	G	A	G	G	8	12356	1	11417-12926
Т	\mathbf{T}	T	${ m T}$	T	T	T	T	С	T	9	12397	1	11417-12926
С	С	С	С	С	С	С	С	С	С	10	12489	\ 1	11417-12926
С	С	С	С	С	С	C	С	С	С	11	12653	#	11417-12926
А	G	G	G	G	G	G	G	G	G	12	14824	1\	14634-16768
Α	Α	Α	Α	Α	G	G	G	A	A	13	14990	1	14634-16768
С	С	С	С	T	С	С	С	С	С	14	15089	1	14634-16768
С	С	C	T	С	С	C	С	С	C	15	15093	1	14634-16768
С	С	T	С	С	С	T	${ m T}$	\mathbf{T}	С	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

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	1.0			NUME			7.0	7.0	0.0		PS	SEQ		REGION
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITI		NO.	EXAMINED
G	G	G	G\	G	G	G	G	G	G	1	3102	1		20-4210
G	G	G	G	\G	G	G	\mathbf{T}	T	T	2	3409	1		20-4210
A	Α	A	A	Æ	G	G	A	A	A	3	3438	1		20-4210
С	С	C	C	9	C	C	С	С	C	4	3603	1		20-4210
G	G	G	G	A\	A	A	А	A	A	5	4054	1		20-4210
G	G	G	G	G \	G	G	A	G	G	6	4082	1		20-4210
С	С	С	\mathbf{T}	С	\c	\mathbf{T}	C	С	С	7	11998	1	11	417-12926
G	G	G	G	G	T	G	G	G	G	8	12356	1	11	417-12926
T	T	T	$_{\mathrm{T}}$	\mathbf{T}	T	\mathbf{T}	\mathbf{T}	T	T	9	12397	1	11	417-12926
С	C	С	С	С	c/	С	C	C	С	10	12489	1	11	417-12926
C	С	T	С	С	c \	C	${f T}$	С	С	11	12653	1	11	417-12926
G	G	G	G	G	G	\G	G	G	G	12	14824	1	14	634-16768
A	G	A	G	A	A	X	A	A	G	13	14990	1	14	634-16768
С	С	С	С	С	С	St.	C	С	С	14	15089	1	14	634-16768
С	С	C	C	C	C	c\	C	С	С	15	15093	1		634-16768
T	Т	Т	Т	C	T	c \	T	T	T	1.6	15529	1	14	634-16768
G	G	G	G	G	G	G	G	A	G	17	15932	1		634-16768
G	G	G	G	G	· G	G	9	G	G	18	16165	. 1	1.4	634-16768
		-	•	_	~	•	1							
		ISO	SENE	NUME	3ERª		PŞ	b		PS	SEQ ID	REG	ION	
21	22	1500 23	SENE 24	NUME 25	BER ^a 26	27	P'S NUM			PS POSITION ^c	SEQ ID		ION MINEC) ^d
21 G	22 G					27 T	- · · I	BER 1				EXA		
		23	24	25	26		- · · I	BER 1 2		POSITIONC	NO.	EXAN 2920	MINEC	. 0
G	G	23 G	24 G	25 G	26 G	T	- · · I	BER 1 2		POSITION ^c 3102	NO.	EXAM 2920 2920	MINEC 0-421	.0
G T	G T	23 G T	24 G T	25 G T	26 G T	T	- · · I	BER 1		POSITION° 3102 3409	NO. 1	EXAM 2920 2920 2920	MINEC 0-421 0-421	.0 .0 .0 .
G T A	G T A	23 G T A	24 G T A	25 G T A	26 G T G	T G G	- · · I	BER 1 2		POSITION ^c 3102 3409 3438	NO. 1 1 1	EXAM 2920 2920 2920 2920	MINEC 0-421 0-421 0-421	.0 .0 .0 .
G T A C	G T A C	23 G T A	24 G T A	25 G T A G	26 G T G	T G G	- · I	BER 1 2		POSITION ^c 3102 3409 3438 3603	NO. 1 1 1 1	EXAM 2920 2920 2920 2920 2920	MINEC 0-421 0-421 0-421 0-421	.0 .0 .0 .0
G T A C A	G T A C A	23 G T A C	24 G T A C	25 G T A G A	26 G T G C	T G G C A	- · I	BER 1 2 4 5		POSITION ^c 3102 3409 3438 3603 4054	NO. 1 1 1 1 1	EXAM 2920 2920 2920 2920 2920	MINED 0-421 0-421 0-421 0-421 0-421	.0 .0 .0 .0 .0
G T A C A G	G T A C A G	23 G T A C A	24 G T A C G	25 G T A G A	26 G T G C A	T G C A G	- · I	BER 1 2 4 5 6		POSITION ^c 3102 3409 3438 3603 4054 4082	NO. 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 2920 1141	MINEC 0-421 0-421 0-421 0-421 0-421	.0 .0 .0 .0 .0 .0
G T A C A G C G	G T A C A G C	23 G T A C A G	24 G T A C G G	25 G T A G A	26 G T G C A G	T G C A G	- · I	BER 1 2 00 4 5 6 7 8		POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356	NO. 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 2920 1141 1142	MINED 0-421 0-421 0-421 0-421 0-421 0-421 17-12	0 0 0 0 0 0 0 926
G T A C A G C G T	G T A C A G C G	23 G T A C A G C	24 G T A C G G C	25 G T A G A G C	26 G T G C A G	TGGCAGCG	- · I	BER 1 2 2 3 4 5 6 7		POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 2920 1141 1142	MINEC 0-421 0-421 0-421 0-421 0-421 17-12	.0 .0 .0 .0 .0 .0 .926 .926
G T A C A G C G T C	G T A C A G C G T	23 G T A C A G C G T	24 G T A C G G C	25 G T A G A G C	26 G T G C A G C G T	T G G C A G C G T C	- · I	BER 1 2 4 5 6 7 8 9		POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 \12489	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 2920 1141 1141 1141	MINEC 0-421 0-421 0-421 0-421 0-421 17-12 17-12	.0 .0 .0 .0 .0 .0 .926 .926
G T A C A G C G T	G T A C A G C G T C	23 G T A C A G C G	24 G T A C G G C G	25 G T A G C G T C	26 G T G C A G C G T	T G G C A G C G T	- · I	BER 1 2 4 5 6 7 8 9 10		POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 2653	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2920 2920 2920 2920 2920 2920 1141 1142 1143	MINEC 0-421 0-421 0-421 0-421 0-421 17-12 17-12 17-12 17-12	.0 .0 .0 .0 .0 .926 .926 .926 .926
G T A C A G C G T C T G	G T A C A G C G T C T	23 G T A C A G C T T	24 G T A C G G C G T C	25 G T A G C G T C	26 G T G C A G C G T C C	T G G C A G C G T C C	- · I	BER 1 2 4 5 6 7 8 9 10 11 12		POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 2920 1141 1141 1141 1141	MINEC 0-421 0-421 0-421 0-421 0-421 17-12 17-12	.0 .0 .0 .0 .0 .926 .926 .926 .926 .926
G T A C A G C G T G T G A	G T A C A G C G T C T G A	23 G T A C A G C G T T G A	24 G T A C G G C G T C T G	25 G T A G A G C G T C T G A	26 TGCAGCGTCCGA	T G G C A G C G T C C G A	- · I	BER 1 2 4 5 6 7 8 9 10 11 12 13		POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 1141 1141 1141 1463 1463	MINEC 0-421 0-421 0-421 0-421 0-421 17-12 17-12 17-12 17-12	.0 .0 .0 .0 .0 .926 .926 .926 .926 .926
G T A C A G C G T C T G A C	G T A C A G C G T C T G A C	23 GTACAGCGTTTGAC	24 G T A C G G C G T C T G A C	25 G T A G A G C G T C T G A C	26 G T G C A G C G T C C G A C	T G G C A G C G T C C G A C	- · I	BER 1 2 3 4 5 6 7 8 9 10 11 12 13 14		POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 1141 1141 1141 1146 1463 1463	MINED 0-421 0-421 0-421 0-421 0-421 17-12 17-12 17-12 17-12 34-16	.0 .0 .0 .0 .0 .926 .926 .926 .926 .926 .926 .9768
G T A C A G C G T C T G A C C	G T A C A G C G T C T G A C C	23 GTACAGCGTTTGACC	24 G T A C G G C G T C T G A C C	25 G T A G A G C G T C T G A C C	26 TGCAGCGTCCGACC	T G G C A G C G T C C G A C C	- · I	BER 1 2 4 5 6 7 8 9 10 11 12 13 14 15		POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15089	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 1141 1141 1141 1146 1463 1463	MINED 0-421 0-421 0-421 0-421 0-421 17-12 17-12 17-12 34-16 34-16	.0 .0 .0 .0 .0 .0 .926 .926 .926 .926 .926 .926 .9768 .768
G T A C A G C G T C T G A C C C	G T A C A G C G T C T G A C C T	23 GTACAGCGTTTGACCT	24 G T A C G G C G T C T G A C C T C T	25 G T A G A G C G T C T G A C C T	26 G T G C A G C G T C C G A C C C	T G G C A G C G T C C G A C C T	- · I	BER 1 2 4 5 6 7 8 9 10 11 12 13 14 15 16		POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15083 15529	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXAM 2920 2920 2920 2920 1141 1141 1141 1146 1463 1463 1463	MINED 0-421 0-421 0-421 0-421 0-421 17-12 17-12 17-12 34-16 34-16 34-16	.0 .0 .0 .0 .0 .926 .926 .926 .926 .926 .926 .968 .768 .768
G T A C A G C G T C T G A C C	G T A C A G C G T C T G A C C	23 GTACAGCGTTTGACC	24 G T A C G G C G T C T G A C C	25 G T A G A G C G T C T G A C C	26 TGCAGCGTCCGACC	T G G C A G C G T C C G A C C	- · I	BER 1 2 4 5 6 7 8 9 10 11 12 13 14 15		POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15089	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2920 2920 2920 2920 2920 1141 1141 1141 1463 1463 1463 1463	MINED 0-421 0-421 0-421 0-421 0-421 17-12 17-12 17-12 34-16 34-16	.0 .0 .0 .0 .0 .0 .926 .926 .926 .926 .926 .926 .926 .926

^aAlleles for isogenes are presented 5' to 3' in each column;

- (b) a second nucleotide sequence which is complementary to the first nucleotide sequence.
- 21. The isolated polynucleotide of claim 20, which is a DNA molecule and comprises both the first and second nucleotide sequences and further comprises expression regulatory elements operably linked to the first nucleotide sequence.
- 22. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 20, wherein the organism expresses a TNFRSF1A protein that is encoded by the first nucleotide sequence.

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.

23. The recombinant nonhuman organism of claim 22, which is a transgenic animal.

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24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the fragment comprises at least 10 nucleotides in one of the regions of SEQ ID NO:1 shown in the table immediately below and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, guanine at PS4, adenine at PS12, thymine at PS14, thymine at PS15, adenine at PS17 and adenine at PS18, wherein the selected polymorphism has the position set forth in the table immediately below:

			ISC	GENE	E NU	MBE	\mathbb{R}^{a}		/	PS	b	PS		SEQ ID	REG	ION	
	1.	2	3 4	5	6	7	8	9	10	NUMB:	ER	POSITI	ONc	NO.	EXA	MINE	D^d
10	G	G	G G	G	G	G	G	G	G	1		3102		1	292	0-42	10
	G	G	G G	G	G	G	G	G	G	\ 2		3409		1	292	0-42	10
	Α	A	A A	A	A	A	Α	Α	A	\ 3		3438		1	292	0-42	10
	С	С	C C	С	С	С	С	С	С	\ 4		3603		1	292	0-42	10
	A	А	A A		A	A	G	G	G	É		4054		1	292	0-42	10
15	G	G	G G		G	G	G	G	G	6		4082		1		0-42	
	С	С	C C	С	С	С	С	С	С	7 🐧	1	11998		1	114	17-1	2926
E-10-10	G	G	G G	G	G	G	A	G	G	8	1	12356		1	114	17-1	2926
F (2)	\mathbf{T}	\mathbf{T}	т т	${f T}$	Т	\mathbf{T}	Т	С	Т	9	1	12397		1	114	17-1	2926
150	С	С	C C	С	С	C	С	С	С	10	1	12489		1	114	17-1	2926
20	С	С	C C	С	С	С	С	С	С	11	1	12653		1	114	17-1	2926
	A	G	G G	G	G	G	G	G	G	12	1	14824		1	146	34-1	6768
197	A	A	A A	. A	G	G	G	A	A	13		14990		1	146	34-1	6768
ensig Ensign	C	С	C C	Т	С	С	С	С	С	14		15089		1.	146	34 - 1	6768
inad Livi	С	C	С Т	С	С	С	C	С	С	15		1,5093		1	146	34-1	6768
25	С	С	T C	С	С	\mathbf{T}	T	T	С	16		15529		1	146	34-1	6768
SS .	G	G	G G	G	G	G	G	G	G	17		15/932		1	146	34-1	6768
1275	G	G	G G	G	G	G	G	G	G	18		16 \ 65		1	146	34-1	6768
			,									1					
£u.i			ISC	GENE	E NU	MBE	R ^a					PS ^b \		PS	SEQ	ID	REGION
30	11	12	2 13	14	1	5 :	16	17	18	19	20	NUMBER		POSITIO	ON^c	NO.	$EXAMINED^\mathtt{d}$
fire	G	G	G	G	G	(G	G	G	G	G	1 \		3102	1	2	920-4210
la de	G	G	G	G	G	(G	G	T	${f T}$	\mathbf{T}	2	\	3409	1		920-4210
2	A	A	A	Α	G	(G	G	Α	A	A	3	1	3438	1		920-4210
	С	С	C	С	С	(C	С	С	С	С	4	1	3603	1		920-4210
35	G	G	G	G	Α	. 2	A	Α	A	A	A	5	1	4054	1		920-4210
	G	G	G	G	G	(G	G	A	G	G	6	1	4082	1		920-4210
	С	С	С	\mathbf{T}	С		C	\mathbf{T}	С	С	С	7		\ 11998	1		1417-12926
	G	G	G	G	G		G	G	G	G	G	8		12356	1		1417-12926
	Т	Т	\mathbf{T}	\mathbf{T}	Т		Γ	T	${f T}$	${f T}$	Т	9		12397	1		1417-12926
40	С	С	C	С	С		C	С	С	С	С	10		12/489	1		1417-12926
	С	С	${ m T}$	С	С	(C	С	Т	С	С	11		128,53	1		1417-12926
	G	G	G	G	G		G	G	G	G	G	12		14824	1		4634-16768
	Α	G	A	G	A	_	A	А	Α	A	G.	13		1499p	1		4634-16768
	C	С	C	С	С		C	С	С.	С	С	14		15089	1		4634-16768
45	С	С	С	С	С		C	С	С	С	С	15		15093	1		4634-16768
	T	T	${\mathbb T}$	T	С		Γ	С	Т	T	\mathbf{T}	16		15529	\ 1		4634-16768
	G	G	G	Ġ	G		G	G	G	A	G	17		15932	$\sqrt{1}$		4634-16768
	G	G	G	G	G	(G	G	G	G	G	18		16165	1	1.	4634-16768
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		ISOG	ENE	NUMB	€R ^a		PS ^b	PS	SEQ ID	REGION
21	22	23	24	25	\$ 6	27	NUMBER	POSITION°	NO.	EXAMINED ^d
G	G	G	G	G	Ġ	T	1	3102	1	2920-4210
\mathbf{T}	T	${f T}$	\mathbf{T}	T	T	G	2	3409	1	2920-4210
A	A	A	Α	A	G \	G	3	3438	1	2920-4210
С	С	С	С	G	c '	\c	4	3603	1	2920-4210
A	A	A	G	А	A	Æ	5	4054	1	2920-4210
G	G	G	G	G	G	ġ	6	4082	1	2920-4210
С	С	С	С	C	С	C/	7	11998	1	11417-12926
G	G	G	G	G	G	G \	8	12356	1	11417-12926
${f T}$	T	\mathbf{T}	\mathbf{T}	${f T}$	T	T	\ 9	12397	1	11417-12926
С	С	${ m T}$	С	C	С	С	10	12489	1	11417-12926
${f T}$	T	${f T}$	T	\mathbf{T}	Ċ	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	12	14824	1	14634-16768
A	Α	A	A	A	A	A	13	14990	1	14634-16768
С	С	C	С	С	С	С	14	15089	1	14634-16768
С	С	С	C	С	C	C	\ 15	15093	1	14634-16768
С	T	${f T}$	\mathbf{T}	\mathbf{T}	С	T	\ 16	15529	1	14634-16768
G	G	G	G	G	G	G	1 7	15932	1	14634-16768
G	G	G	G	G	G	A	18	16165	1	14634-16768

^aAlleles for isogenes are presented 5' to 3' in each column;

25. An isolated polynucleotide comprising a TNFRSF1A coding sequence, wherein the coding sequence is selected from the group consisting of 8, 9, 14, 17, and 19 shown in the table immediately below, and wherein each of the coding sequences comprises SEQ ID NO:2, except at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

Isog	ene	Coding	Sequence	Number	PS	PS \
8	9	14,17	19		Number	Position
С	С	T	C		7	224
A	G	G	G·		8	362
${f T}$	С	${f T}$	T		9	403
G	G	G	A		17	935

^aAlleles for the isogene coding sequence are presented 5' to 3' in each column; the numerical portion of the isogene coding sequence number represents the number of the parent full TNFRSF1A isogene;

- 26. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 25, wherein the organism expresses a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) protein that is encoded by the polymorphic variant sequence.
- 27. The recombinant nonhuman organism of claim 26, which is a transgenic animal.
- 28. An isolated fragment of a TNFRSF1A cDNA, wherein the fragment comprises adenine at a

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

^dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:2.

- position corresponding to nucleotide 935 in SEQ ID NO:2.
- An isolated polypeptide comprising an amino acid sequence which is a polymorphic variant of a reference sequence for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) protein, wherein the reference sequence comprises SEQ ID NO:3, except the polymorphic variant comprises lysine at a position corresponding to amino acid position 312.
- 30. An isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide of claim 29.
- 31. A method for screening for drugs targeting the isolated polypeptide of claim 31 which comprises contacting the TNFRSF1A polymorphic variant with a candidate agent and assaying for binding activity.
- 32. An isolated fragment of the TNFRSF1A polypeptide, wherein the fragment comprises lysine at a position corresponding to amino acid position 312 in SEQ ID NO:3.
- A computer system for storing and analyzing polymorphism data for the tumor necrosis factor receptor superfamily, member 1A gene, comprising:
 - (a) a central processing unit (CPU);
 - (b) a communication interface;
 - (c) a display device;
 - (d) an input device; and
 - (e) a database containing the polymorphism data;

wherein the polymorphism data comprises any one or more of the haplotypes set forth in the table immediately below:

10				HA.	PLO'	TYPI	E N	UMBI	EŘ₹		PS ^b	PS
garene g	1	2	3	4	5	6	7	8	9`	10	NUMBER	${\tt POSITION}^{\tt c}$
	G	G	G	G	G	G	G	G	G	G	1	3102
	G	G	G	G	G	G	G	G	G	G `	2	3409
	A	A	Α	A	Α	A	A	A	A	Α	3	3438
15	C	C	С	C	С	С	С	С	С	С	4	3603
	A	A	Α	A	Α	A	A	G	G	G	5	4054
	G	G	G	G	G	G	G	G	G	G	6	4082
	С	С	С	С	С	С	С	С	С	С	7	11998
	G	G	G	G	G	G	G	A	G	G	8	12356
20	Т	Т	\mathbf{T}	${ m T}$	\mathbf{T}	${f T}$	${f T}$	\mathbf{T}	С	${f T}$	9	12397
	С	С	С	C	С	С	С	C	С	С	10	12489
	C	С	\mathbb{C}_{-1}	С	С	С	С	С	С	C	11	12653
	A	G	G	G	G	G	G	G	G	G	12	14824
	A	Α	A	A	Α	G	G	G	Α	Α	13	14990
25	С	С	С	С	${f T}$	С	С	С	С	C	14	15089
	C	С	С	\mathbf{T}	С	С	С	С	С	С	15	15093
	С	С	\mathbf{T}	С	С	С	\mathbf{T}	\mathbf{T}	T	С	16	15529
	G	G	G	G	G	G	G	G	G	G	17	15932
	G	G	G	G	G	G	G	G	G	G	18	16165

30

The state of the s

30	\													
			HA	PLOT	YPE	NUMB	ER ^a					$\mathtt{PS}^\mathtt{b}$	PS	
	11	12	13	14	15	16	17	18	19	20	NU	MBER	POSITION°	
	G `	G	G	G	G	G	G	G	G	G		1	3102	
	G	Ġ/	G	G	G	G	G	\mathbf{T}	${f T}$	T		2	. 3409	
35	A	A	Λ	A	G	G	G	A	A	A		3	3438	
	C	С	ß	С	С	C	С	С	C	С		4	3603	
	G	G	G\	G	A	A	A	A	A	A		5	4054	
	G	G	G `	\G	G	G	G	A	G	G		6	4082	
	Ċ	С	С	R	С	С	T	С	C	С		7	11998	
40	G	G	G	G	G	G	G	G	G	G		8	12356	
	${f T}$	\mathbf{T}	${f T}$	${f T}$	T	T	T	T	\mathbf{T}	T		9	12397	
	С	С	C	С	9/	С	С	С	С	С		10	12489	
	С	С	${ m T}$	С	C \	∖ C	С	T	С	С		11	12653	
	G	G	G	G^{-}	G	Ğ	G	G	G	G		12	14824	
45	A	G	A	G	A	A	A	A	A	G		13	14990	
	С	С	С	С	С	C `	\c	С	С	С		14	15089	
	С	С	С	С	С	С	Ġ.	С	С	С		15	15093	
	T	\mathbf{T}	Т	Т	С	T	C	\mathbf{T}	Т	\mathbf{T}		16	15529	
xiam.	G	G	G	G	G	G	G	G	A	G		17	15932	
50	G	G	G	G	G	G	G	Ġ	G	G		18	16165	
The state of the same state of								/						
in and			HA	PLOT	YPE	NUMB	ERa		\ 1	?S ^b		PS		
eijas 1 das	21	22	23	24	25	26	27.		1	NUMBI	ΞR	POSI	$TION^{c}$	
£21 }	G	G	G	G	G	G	$^{\mathrm{T}}$		/-	Į.		3102		
55	${f T}$	T	T	\mathbf{T}	T	T	G			2		3409		
South S SPE	A	A	A	A	A	G	G			3 \		3438		
	С	С	С	C	G	С	С			$4 \setminus$		3603		
\$400E	A	A	A	G	A	A	A		į	ō		4054		
60	G	G	G	G	G	G	G			6		4082		
60	С	С	C	C	C	C	С			7	\	1199		
4/4/ 4 s	G	G	G	G	G	G	G			3		1235		
luci.	${f T}$	${f T}$	${ m T}$	${f T}$	\mathbf{T}	T	${f T}$			9		1239		
	С	С	${\mathtt T}$	С	С	C	C ·			10		1248		
ALL S	${f T}$	\mathbf{T}	${ m T}$	T	T	С	С			11		1265	3	
65	G	G	G	G	G	G	G			12		1482	4	
	A	A	A	A	A	A	A			13		1499	0 \	
	С	С	С	С	С	С	С			14		1508	9	
	С	С	С	С	С	С	С			15		1509	3	
	С	${f T}$	${f T}$	${f T}$	\mathbf{T}	С	T			16		1552	9	
70	G	G	G	G	G	G	G			17		1593		
	G	G	G	G	G	G	A			18		1616	5 M	
		^a All	eles f	or hap	lotype	es are	presen	ted 5'	to 3'	in eacl	n col		,/	
		^b PS	= pol	ymor	hic si	te;	^					•		/

the haplotype pairs set forth in the table immediately below:

^bPS = polymorphic site; ^cPosition of PS in SEQ ID NO:1;

\									h-	
		CYPE PA							PS ^b	PS
	12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION°
80	∕G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
	ĠXG	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
	c/c \	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
	G/G	$A \setminus A$	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
85	G/G	G/Œ	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
	C/C	C/C \	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
	G/G	G/G	`G/G	G/G	G/G	G/G	G/G	G/G	8	12356
	T/T	T/T	TXT	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C/	C/C	C/C	C/C	C/T	C/C	10	12489
90	C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
	G/G	A/A	A/A	A/G\	G/A	A/A	A/A	A/A	13	14990
	C/C	C/C	C/C	C/C	√C/C	C/C	C/C	C/C	14	15089
	C/C	C/C	C/C	C/C	çχc	C/C	C/C	C/C	15	15093
95	T/T	T/T	C/C	T/T	\mathbb{T}/\mathcal{C}	C/C	T/T	C/T	16	15529
Aug and	G/G	G/G	G/G	G/G	G/G \	G/G	G/G	G/G	17	15932
2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	G/G	G/G	G/G	G/G	G/G	∖G / G	G/G	G/G	18	16165
1205						\mathcal{A}			1-	
- 20-00-pa	LIZ DT.∩⊓	TYPE PA	тра			1			PS ^b	PS
2500 2500						. 1				
100	2/19	3/14	12/1	5 22/8	2/9	3/21	2/15	12/17	NUMBER	POSITIONC
	2/19 G/G	3/14 G/G	12/1: G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION ^c 3102
L.F.	2/19 G/G G/T	3/14 G/G G/G	12/1: G/G G/G	G/G T/G	G/G G/G	G/G G/T	G/G G/G	G/G G/G	NUMBER 1 2	POSITION ^c 3102 3409
ut Ev	2/19 G/G G/T A/A	3/14 G/G G/G A/A	12/19 G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/G G/T A/A	G/G G/G A/G	G/G G/G A/G	NUMBER 1 2 3	POSITION ^c 3102 3409 3438
Harry Board Branch	2/19 G/G G/T A/A C/C	3/14 G/G G/G A/A C/C	12/15 G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G G/T A/A C/C	G/G G/G A/G C/C	G/G G/G A/G C/C	NUMBER 1 2 3 4	POSITION ^c 3102 3409 3438 3603
105	2/19 G/G G/T A/A C/C A/A	3/14 G/G G/G A/A C/C A/G	12/15 G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C A/G	G/G G/T A/A C/C A/A	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054
105 105	2/19 G/G G/T A/A C/C A/A G/G	3/14 G/G G/G A/A C/C A/G G/G	12/15 G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/G G/T A/A C/C A/A G/G	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054 4082
105 105	2/19 G/G G/T A/A C/C A/A G/G C/C	3/14 G/G G/G A/A C/C A/G G/G C/T	12/19 G/G G/G A/G C/C G/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/G C/C G/A G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998
105	2/19 G/G G/T A/A C/C A/A G/G C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/18 G/G G/G A/G C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G	G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356
Total such states and such such such such such such such such	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G	12/15 G/G G/G A/G C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/A T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C G/A G/G C/T G/G	NUMBER 1 2 3 4 5 6 7 8 9	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397
105	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
Total such states and such such such such such such such such	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	12/18 G/G G/G A/G C/C G/A G/G C/C G/C C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
Total such states and such such such such such such such such	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G T/T C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
Total such states and such such such such such such such such	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C C/C G/G A/A	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A	G/G G/G A/G C/C G/A G/G C/T C/C C/C G/G G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
105	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G C/C	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/G A/A C/C	G/G G/G A/G C/C A/A G/G C/C G/G C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G T/T C/C G/G G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
Total such states and such such such such such such such such	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G C/C	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C C/C G/A C/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G C/C	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/T G/G A/A C/C C/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	G/G G/G A/G C/C G/A G/G T/T C/C C/C G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
105	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C C/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G C/C T/T	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/A C/C C/C T/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G C/C T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/A G/G T/T C/C G/G G/A C/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
105	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C C/T G/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G C/C T/T G/G	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G C/C C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G A/G C/C C/C G/C	G/G G/G A/A C/C A/G G/C C/C G/G A/A C/C C/C G/G A/A C/C C/T G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/C C/C G/G T/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C G/G	G/G G/G A/G C/A G/G G/T C/C G/G G/A C/C G/G G/A C/C G/G G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
105	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C C/T	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C C/C G/G A/G C/C T/T	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/A C/C C/C T/C	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C T/C G/G A/G C/C T/T	G/G G/G A/A C/C A/G G/G C/C G/G T/C C/C G/G A/A C/C C/C	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/T G/G A/A C/C T/C	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/G A/G C/C G/A G/G T/T C/C G/G G/A C/C T/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
105	2/19 G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C C/T G/A	3/14 G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C G/G A/G C/C T/T G/G	12/18 G/G G/G A/G C/C G/A G/G C/C G/G T/T C/C G/G C/C C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A T/T C/C G/G A/G C/C C/C G/C	G/G G/G A/A C/C A/G G/C C/C G/G A/A C/C C/C G/G A/A C/C C/T G/G	G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C G/G A/C C/C G/G T/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C C/C G/G	G/G G/G A/G C/A G/G G/T C/C G/G G/A C/C G/G G/A C/C G/G G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

120	HAPLOTYPE PAIR ^a PS ^b PS											
	2/21	22/3	22/25	5 12/25	12/24	12/13	3/16	22/16	NUMBER	${\tt POSITION}^{\tt c}$		
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102		
	G/T	T/G	T/T	G/T	G/\mathtt{T}	G/G	G/G	T/G	2	3409		
	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438.		
125	C/C	cye	C/G	C/G	C/C	C/C	C/C	C/C	4	3603		
	A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054		
	G/G	G/G	\g/G	G/G	G/G	G/G	G/G	G/G	6	4082		
	C/C	C/C	cxç	C/C	C/C	C/C	C/C	C/C	7	11998		
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356		
130	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397		
100	C/C	C/C	C/C	c/g	C/C	c/c	C/C	C/C	10	12489		
	C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653		
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824		
	A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990		
135	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089		
100	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093		
	C/C	T/T	T/T	T/T	T/T	TXT	T/T	T/T	16	15529		
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932		
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165		
140	0, 0	0, 0	0,0	0, 0	0, 0	0,0 (À	0, 0				
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	HAPLO	LABE DA	IR~				• - /		PS ^o	PS		
15		TYPE PA 22/10		2/26	22/11	12/7	. /	22/18	PS ^b NUMBER	PS POSITION ^C		
See See Mark Mark Mark Mark Mark Mark Mark Mark	3/27	22/10	2/16	2/26 G/G	22/11 G/G	12/7 G/G	22/2	22/18 G/G	NUMBER	POSITION		
	3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	G/G	22/2 G/G	G/G	NUMBER 1	POSITION ^c 3102		
	3/27 G/T G/G	22/10 G/G T/G	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	22/2 G/G T/G	G/G T/T	NUMBER 1 2	POSITION ^c 3102 3409		
145	3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G A/A	22/2 G/G T/G A/A	G/G T/T A/A	NUMBER 1 2 3	POSITION ^c 3102 3409 3438		
145	3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	22/2 G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3 4	POSITION ^c . 3102 3409 3438 3603		
The state of the s	3/27 G/T G/G A/G C/C A/A	22/10 G/G T/G A/A C/C A/G	2/16 G/G G/G A/G C/C A/A	G/G G/T A/G C/C A/A	G/G T/G A/A C/C A/G	G/G G/G A/A C/C G/A	22/2 G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3 4 5	POSITION ^c 3102 3409 3438 3603 4054		
1 de la company	3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C G/A G/G	22/2 G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5 6	POSITION ^c 3102 3409 3438 3603 4054 4082		
	3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C G/A G/G C/C	22/2 G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3/27 G/T G/G A/G C/C A/A G/G C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G	22/2 G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T AXA C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 6 7	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/G C/C G/G T/T	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 7 8 9	POSITION ^c .3102 3409 3438 3603 4054 4082 11998 12356 12397		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 7 8 9 10	POSITION ^c .3102 3409 3438 3603 4054 4082 11998 12356 12397 12489		
1	3/27 G/T G/G A/G C/C A/A G/G C/C G/C C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	G/G G/G A/A C/C G/A G/G C/C G/G T/T C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/T A/A C/C A/A G/A C/C G/G T/T C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653		
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G G/T A/G C/C A/A G/G C/C G/G T/T C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G	G/G G/G A/A C/C G/A G/C C/C G/G T/T C/C G/G	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C	G/G T/T A/A C/C A/A C/C G/G T/T C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824		
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	2/16 G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/G A/A	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A	G/G G/G A/A C/C G/G C/C G/G T/T C/C G/G G/G	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C G/G A/A	G/G T/T A/A C/C A/A C/C G/G T/T C/C T/T G/G A/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990		
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/G A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	2/16 G/G G/G A/G C/C A/A G/C G/G T/T C/C G/G A/A C/C	G/G G/T A/G C/C A/A G/C G/G T/T C/C G/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G G/G A/A C/C G/A G/C G/G T/T C/C G/G G/C C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/T A/A C/A G/A C/C G/G T/T C/T G/A C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089		
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/C A/A G/C G/G T/T C/C G/A C/C	G/G G/T A/C A/C G/C G/C T/C C/C G/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/A C/C G/A C/C G/C G/C C/C C/C C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/TA C/A C/A C/G T/C T/T G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093		
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C C/C T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C T/C	2/16 G/G G/G A/A G/C C/C G/G T/T C/C G/A C/C C/T	G/G G/T A/C A/A G/C G/G T/T C/C G/A C/C C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C T/T	G/G G/A C/C G/A G/C G/C G/C C/C G/C C/C T/T	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C C/C T/C	G/G T/T A/A C/A G/A G/C G/G T/T C/C T/T G/A C/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529		
	3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T C/C G/C A/A C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C T/C G/G A/A C/C C/C	2/16 G/G G/G A/C A/A G/C G/G T/T C/C G/A C/C	G/G G/T A/C A/C G/C G/C T/C C/C G/A C/C	G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C G/G A/A C/C C/C	G/G G/A C/C G/A C/C G/C G/C C/C C/C C/C	22/2 G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C T/C G/G A/A C/C	G/G T/TA C/A C/A C/G T/C T/T G/A C/C C/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION ^c 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093		

1	HAPLOI	YPE PA	.IR ^a				PS ^b	PS
	22×12	12/5	12/3	12/2	14/6	16/4	NUMBER	$POSITION^{c}$
	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
165	T/G	\G/G	G/G	G/G	G/G	G/G	2	3409
	A/A	AXA	A/A	A/A	A/A .	G/A	3	3438
	C/C	C/C/	C/C	C/C	C/C	C/C	4	3603
	A/G	G/A	G/A	G/A	G/A	A/A	5	4054
	G/G	G/G	GΧG	G/G	G/G	G/G	6	4082
170	C/C	C/C	c/c/	C/C	T/C	C/C	7	11998
	G/G	G/G	G/G	Ğ√G	G/G	G/G	8	12356
	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	c/c \	C/C	C/C	10	12489
	T/C	C/C	C/C	C/C	J&\C	C/C	11	12653
175	G/G	G/G	G/G	G/G	G/&	G/G	12	14824
	A/G	G/A	G/A	G/A	G/G \	A/A	13	14990
	C/C	C/T	C/C	C/C	C/C	<i>g</i> √c	14	15089
	C/C	C/C	C/C	C/C	C/C	C /T	15	15093
	T/T	T/C	T/T	T/C	T/C	T/C \	1 6	15529
180	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
and The	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

^aHaplotype pairs are represented as 1st Haplotype/2nd Haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column; ^cPosition of PS in SEQ ID NO:1;

and the frequency data in Tables 6 and 7.

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34. A genome anthology for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene which comprises two or more TNFRSF1A isogenes selected from the group consisting of isogenes 1-27 shown in the table immediately below, and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

	ISOGENE NUMBERa										PS ^b	PS	SEQ ID	REGION
	1	2	3	4	5	6	7	8	9	10	NUMBER	POSITIONC	NO.	$EXAMINED^d$
10	G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
	G	G	G	G	G	G	G	G	G	G	2	3409	1	2920-4210
	A	Α	Α	Α	Α	A	A	A	Α	A	3	3438	1	2920-4210
	С	С	С	С	С	С	С	С	С	С	4	3603	1	2920-4210
	Α	A	Α	A	Α	A	A	G	G	G	5	4054	1	2920-4210
15	G	G	G	G	G	G	G	G	G	G	6	4082	1	2920-4210
	С	С	С	C	C	С	С	С	С	С	7	11998	1	11417-12926
	G	G	G	G	G	G	G	Α	G	G	8	12356	1	11417-12926
	Т	Т	\mathbf{T}	Т	${ m T}$	${ m T}$	T	T	С	${ m T}$	9	12397	1	11417-12926
	С	С	С	С	С	С	С	С	С	С	10	12489	1	11417-12926
20	С	С	С	С	C	С	С	С	С	C	11	12653	1	11417-12926
	A	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
	A	A	Α	A	Α	G	G	G	A	A	13	14990	1	14634-16768
	C	С	С	С	Т	С	С	С	С	С	14	15089	1	14634-16768
	С	С	С	T	С	С	С	С	С	С	15	15093	1	14634-16768
25	С	С	\mathbf{T}	С	С	С	\mathbf{T}	\mathbf{T}	\mathbf{T}	С	16	15529	1	14634-16768
	G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
	G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

30	11	12	13	GENE 14	15	16	17	18	19	20	PS ^b NUMBER	PS POSITIO		NO.	REGION EXAMINED ^d	
	G	G	G	G	G	G	G	G T	G	G	1	3102 3409	1 1 ·		920-4210	
	G A	G A	G A	G A	G G	G G	G G	T A	T A	T A	2 3	3409	1		920-4210 920-4210	
	C	C	C	C	C	C	C	C	C	C	4	3603	1		920-4210	
35	G	G	G	G	A	A	A	A	A	A	5	4054	1		920-4210	
22	G	G	G	G	G	G	G	A	G	G	6	4082	1		920-4210	
	C	C	Č	T	C	C	T	C	C	C	7	11998	1		1417-12926	
	Ğ	Ğ	Ğ	G	G	Ğ	G	Ğ	Ğ	Ğ	8	12356	1		1417-12926	
	Т	T	T	T	T	T	T	Τ-	Т	\mathbf{T}	9	12397	1	1	1417-12926	
40	С	C	C	С	С	С	С	С	С	С	10	12489	1	1	1417-12926	
	C	С	T	С	С	С	C	T	С	С	11	12653	1	1	1417-12926	
	G	G	G	G	G	G	G	G	G	G	12	14824	1	1	4634-16768	
	Α	G	A	G	A	A	A	Α	A	G	13	14990	1	1	4634-16768	
	C	C	C	C	C	C	C	С	С	C	14	15089	1	1.	4634-16768	
45	C,	С	C	С	С	С	С	С	C	C	15	15093	1	1.	4634-16768	
	\mathbf{T}	\mathbf{T}	\mathbf{T}	${ m T}$	С	T	С	${f T}$	${ m T}$	\mathbf{T}	16	15529	1		4634-16768	
	G	G	G	,G	G	G	G	G	A	G	17	15932	1		4634-16768	
	G	$G_{_{1}}$	G	G	G	G	G	G	G	G	18	16165	1	1	4634-16768	
						a			- h							
To the state of th	0.1	0.0	ISOC		NUMI		0.7	PS			PS	SEQ ID	REG		nd.	
127	21	22	23	24	25	26	27	NON	IBER		POSITION°			MINE 0-42		
353	G T	G T	G T	G T	G T	G T	T G		1 2	•	3102 3409	1 1		0-42		
181	A	A	A	A	A	G G	G		3		3438	1		0-42		
55	C	C	C	C	G	C	C		3 4		3603	1		0-42		
	A	A	A	G	A	A	A		5		4054	1		0-42		
ingi ing	·G	G	G	G	G	G	G		6		4082	1		0-42		
	C	C	C	C	C	C	C		7		11998	1		17-1		
ener E	G	G	Ğ	G	G	G	Ğ		8		12356	1		17-1		
60	T	T	Ť	$\overset{\circ}{\mathrm{T}}$	T	T	T		9		12397	1		17-1		
QĮ	Ĉ	Ĉ	T	Ĉ	Ĉ	Ĉ	Ĉ		10)	12489	1		17-1		
L	T	$\bar{\mathrm{T}}$	${ar{ ext{T}}}$	Т	T	Č	C		11		12653	1		17-1		
reils.	G	G	G	G	G	G	G		12		14824	1		14634-16768		
to S	A	A	A	A	A	A	A		13		14990	1	146	34-1	6768	
65	C	С	С	С	С	С	С		14		15089	1	146	34-1	6768	
	C	С	C	С	С	С	С		15	5	15093	1	146	34-1	6768	
	C	T	T	T	T	С	T		16	5	15529	1	146	34-1	6768	
	G	G	G	G	G	G	G		17		15932	1		34-1		
	G	G	G	G	G	G	A		18	}	16165	1	146	34-1	6768	
70		a .														

^aAlleles for isogenes are presented 5' to 3' in each column;

^bPS = polymorphic site;

^cPosition of PS in SEQ ID NO:1;

^dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.